



FIGURE 1A

SEQ ID NO: 41	M-----GHGGE-----GMSLEFPTWVAVGVCTVIVAISLAVERLLH	1
SEQ ID NO: 40	MITRSRCRRSLLWFLVFHGGATATGAPSGGKELSQPTWAVAVVCTFLILISHLLEKGLQ	
SEQ ID NO: 39	M-----SDKKG-VPARELPETPSWAVAVVFAAMVLVSVLMEHGLH	
SEQ ID NO: 42	M-----ADQ---VKEKTEETSTWAVAVVCFVLLLSIVIEKLIH	
SEQ ID NO: 08	M-----SGGEE-----GATLEFPTWVVAACFTVIVAISLAAERLLH	
SEQ ID NO: 12	M-----AGESSSSRDLDDQPTWAVAAVCTVFILVSIKESLH	
SEQ ID NO: 14	M-----GGGEE-----GNNLEFPTWVAVVCSVIVAASFAAERFLH	
SEQ ID NO: 28	M-----GG-----KTLQETPTWAVAVVCFVLLSISILIEHILH	
SEQ ID NO: 32	M-----AEDYEYPPARTLPETPSWAVAVVFAVMIIIVSVLLEHALH	
SEQ ID NO: 38	M-----AGGGGK-----AKPLEYPTWIVAVVCSVMIIISLLFERLLH	60
		1
SEQ ID NO: 41	YFGTVLKKKKOKPLYEALQKVKEELMLLGFISLLLTVFQGL-ISKFCVKENVLMHMLPCS	
SEQ ID NO: 40	RLANWLWKKHKNSLLEALEKIKAEMLILGFISLLLTIGE-PYILKICVPRKAALSMLPCL	
SEQ ID NO: 39	KLGHWFQHRHKKALWEALEKMKAEMLVGFISLLLIQTQDPIIAKICISEDAADVMPCK	
SEQ ID NO: 42	KIGSWFKKKNKKALYEALQKKEELMLMGFISLLLTIGQG-YISNICIPKNIASMHPCS	
SEQ ID NO: 08	YGGKFLKAKDQKPLYEALQKKEELMLLGFISLLLTVTQNG-ITKICVRPSLTLMHMLPCN	
SEQ ID NO: 12	KVGTWLGQKKKKALLEALEKVKAELMILGFISLLLTFGQ-SYIVRICIPEKLADNMLPCP	
SEQ ID NO: 14	YGGKFLKRKNQKPLYEALQKKEELMLLGFISLLLTITQNG-IIRICVPVGWTHHMLPCS	
SEQ ID NO: 28	LIGKWLKHKHKKRAICEALEKIKSELMMLLGFISLLLTIGQG-LISRICISEKVAGTFHPCP	
SEQ ID NO: 32	KLGHWFHKKRKNALAEALEKIKAEMLVGFISLLLAQTQDPIG-ICISEKAASIMRPCS	
SEQ ID NO: 38	RLGKRRLIRSRKKPLYEALLKVKEELMLLGFISLLLTVFQGP-MGKVCVSPSAMLHLQPCCK	120
		61

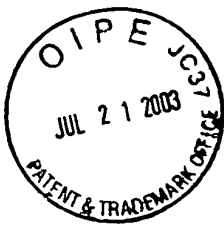


FIGURE 1B

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SEQ ID NO:41 LDSR-----REAGASEHKNVTAKEHFQTFPIVG-TTRLLAEH-----AAVQVGYCSEK
SEQ ID NO:40 -----SEDTVLFQKLAPSSL-----SRHLLAAGDTSIN-----C-KQ
SEQ ID NO:39 RGTEGRK-----PSKYVDY-----CPE-
SEQ ID NO:42 ASEEARKYGKDVPKDEEENLRKLLQLVDS--LIPRRSLATKGYD-K-----CAEK
SEQ ID NO:08 LHD-----APANHES-----HFQTFP--G-TARRLLSGEHSTPESASKIGYCSRK
SEQ ID NO:12 Y-----KY-KEDKKASDSEEHRRKLLSY-----ERRYLAADTTSEK-----CSRE
SEQ ID NO:14 L-----
SEQ ID NO:28 -----KYYKKKEESEHRTNNGRRLLAAFLDSDNQNHRRILAAAGGD-N-----CPP-
SEQ ID NO:32 LPPGSVK-----SKYDYY-----CAKK
SEQ ID NO:38 -----PPPHETDHLGD-----AVFTGVLG-GARRLLAGGASSDK-----YCLKK
121 180

SEQ ID NO:41 GKVPLLSLEALHHLHIFIVLAISHVTFCVLTVIFGSTRIHQWKKWEDSIADEKFDPEA
SEQ ID NO:40 GSEPLITLKGHLHILLFFLAIFHIVYSLITMMLSRKIRGWKKWEQETLSNDYEFSD
SEQ ID NO:39 GKVALMSTGSLHQLHVFIFVLAVFHVTVYSVITIALSRKMRWKKWETETTSLEYQFAND
SEQ ID NO:42 GKVAFVSAYGMHQLHIFIFVLAVCHVIYCIYVYALGKTKMRWKKWEEETKTIEYQYSHD
SEQ ID NO:08 HKVPLLSVEALHHLHIFIFVLAVVHVSFSVLTVVFGGARIRQWKHWEDSIAKQNYETDRV
SEQ ID NO:12 GHEPLLSVNGLHQLHILRILLAVIHVLYSAITMMLGLRLKILGWKAWAAGLQLHNYEFANA
SEQ ID NO:14 -----
SEQ ID NO:28 GKVPFVSSEGIHQLHIFIFVLAVFHVLYCILTALGRAKMRWKKWEEETKTAQYQFSHD
SEQ ID NO:32 GKVSLMSTGSLHQLHIFIFVLAVFHVTVYSVIMALSRLKMRWKKWETETASLEYQFAND
SEQ ID NO:38 DKVPLLSDDAIHQLHIFIFVLAVTHFLLSAITVLLGMAQTRNWRHWETKIQENNGSAPQM
181 240
```




FIGURE 1D

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SEQ ID NO:41 LLAVGTTKLEHVIAQLAHEVAEKHVAIEGDLVVKPSDEHFWFSKPQIVLYLIHFILFQNAF
SEQ ID NO:40 ILAVGTTKLQAIMATMALEIIVETHAVVQGMPLVQSGDRYFWDPCQLLLHLIHFALFQNAF
SEQ ID NO:39 LLCVGTKLEMIIMEMALEIQDRASVIKGA PVVEPSNKF FWHFRPDWVLF FFIHLTLFQNAF
SEQ ID NO:42 ILIVGTTKLQVITTKLGLRIQEKGDVVKGTPLVQPGDHHFFWFGFRPRFIFLFIHLVLTNAF
SEQ ID NO:08 LLAVGTTKLEHIIITQLAHEVPEKHAALIEGDLVVPSPDEHFWFHRPHVVFLFIHLFQNAF
SEQ ID NO:12 ILAVGTTKLQAILANMALEITERHAVVQGMPLVQSGDKYFWFGQPQLVHLIHFALFQNAF
SEQ ID NO:14 -----
SEQ ID NO:28 -----
SEQ ID NO:32 LLCVGTKLEMIIMEMALEIQDRASVIKGA PVVEPSNKF FWHFRPDWVLF FFIHLTLFQNAF
SEQ ID NO:38 LLMVGSKMEHIIITELAYEVAQKHTAIRGDLVVSPSDNFFWFHFRPKLVLLLIIHIVL FQNAF
361
SEQ ID NO:41 EIAFFFWI WVTYGFDSCIMGQVRYIVPRLVIGVFIQVLCYSTLP LYAIVSQMGSSFKKA
SEQ ID NO:40 QITHFFWIWYSFGLKSCFHKDFNLVVS KLFLCLGALILCSYITLP LYALVTQMGS HMKKA
SEQ ID NO:39 QMAHFVWTVATPGLKKCYHTQIGLSIMKV VVGLALQFLCSYMTFPL YALVTQMGSNMKRS
SEQ ID NO:42 QLAFFVWSTYEFGLKNCFHESRVDVIRISIGLLVQILCSYVTLPL YALVTQMGSKMKPT
SEQ ID NO:08 EIAFFFWI WVTYGFDSCIMGQVRYIVPRLVIGVFIQVLCYSTLP LYAIVTQMGT HYKRA
SEQ ID NO:12 QITYILWIWYSFGLRNCFR TDYKLA VVKVALXM-MLCLCSYITLP LYALVTQMGS RMKTA
SEQ ID NO:14 -----
SEQ ID NO:28 ---FFA-----
SEQ ID NO:32 QMAHFVWTVATPGLKKCFHMHIGLSIMKV VVGLALQFLCSYITFPL YALVTQMGSNMKRS
SEQ ID NO:38 EIAFFFWI WVTYGFKSCIMGKPAYVITRVVISVICQVLCGYSTLP LYAVVSHMGNSFKKT
421
480
```



FIGURE 1E

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SEQ ID NO:41 IFEENVQVGLVGVGWAQKVQKRDILKAAA-----SNGDEGSSQAGPGPDGSGS-----
SEQ ID NO:40 VFDEQMAKALKKKWHKDIKLLK-----GKARKLPSKTLGVSEFSL-----
SEQ ID NO:39 IFDEQTSKALTNRNRTAKEKKKVRDMDMLMAQMIGDATPSRGSSPMPSRGSSPVHLLHKG
SEQ ID NO:42 VFNERVATALKSWHHTA--KKNIKH-----GRTSESTTFFSSRPTTPTHGSSPIHLLRNA
SEQ ID NO:08 IFNDHLQNIIVGWAQKAKKRKGLKA-----DGNPGQGSSQESAN-----
SEQ ID NO:12 IFDEQTNKALKKKWHMAAKKKQ-----GGAUTLGKSSARIMDGSP-----
SEQ ID NO:14 -----KDKKK-----
SEQ ID NO:28 -----
SEQ ID NO:32 IFDEQTAKALTNRNRTAKEKKKVRDMDMLMAQMIGDATPSRGTSMPMSRASSPVHLLHKG
SEQ ID NO:38 IFDENVTGLVNWAEKA--RRGTRTPN-----KITTDASSSPIDEANGGA-----
481
SEQ ID NO:41 -----APAAGPGAGFAGIQLSRVTRNNAGDTNNEITPDHN-----N-----
SEQ ID NO:40 -----SSSSATTLHRSKTTGH-----SSNIYYKQEEDEEMSD--L-----
SEQ ID NO:39 ---MGRSDD-----QSAPTSPTQOEARMYPVVVAHPVHRLNPNDRRRSASSSAL
SEQ ID NO:42 PHKRSRVDESFAVSFSPRNSDFDSWDPESQHETAETSNHRSRFGEESEKFKVSSSV
SEQ ID NO:08 -----TGIQLGSIFFKATAPGDSSSAPKADGISSV.-----
SEQ ID NO:12 -----GNSSTVHSLAPHYTVSKLLATQPAPHQQRTRIKIKIMN--M-----
SEQ ID NO:14 -----K-----
SEQ ID NO:28 -----
SEQ ID NO:32 ---MGRSDD-----QSAPTSPTMEEARMYPVVVAHPVHRLNPADRRRSVSSSAL
SEQ ID NO:38 -----VQMT-----NTRANSVEQGTARLI.-----
600
```



FIGURE 1F

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SEQ ID NO:41 -----
SEQ ID NO:40 EAGAEDAIDRIQQEMQF-----HNS
SEQ ID NO:39 E-----ADIPSADFSFSQ-G
SEQ ID NO:42 ELPPGPGQIRTQHEISTISLRDFSFKR--
SEQ ID NO:08 -----
SEQ ID NO:12 NPMVLSCLRWRKQQASL.-----
SEQ ID NO:14 -----
SEQ ID NO:28 -----
SEQ ID NO:32 D-----ADIPSADFSFSQG.
SEQ ID NO:38 -----
601
629
```